

## 09806087 Results

SEQ ID NO: 2

## SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	148.2	12.4	2732	1	US-08-476-000-60	Sequence 60, Appl
2	148.2	12.4	2732	1	US-08-472-840-60	Sequence 60, Appl
3	148.2	12.4	2732	2	US-08-476-976-60	Sequence 60, Appl
4	148.2	12.4	2732	3	US-08-474-410-60	Sequence 60, Appl
5	148.2	12.4	2732	3	US-08-486-673B-60	Sequence 60, Appl
6	146.6	12.3	1475	1	US-08-097-938-1	Sequence 1, Appli
7	146.6	12.3	1475	1	US-08-476-000-1	Sequence 1, Appli
8	146.6	12.3	1475	1	US-08-472-840-1	Sequence 1, Appli
9	146.6	12.3	1475	2	US-08-476-976-1	Sequence 1, Appli
10	146.6	12.3	1475	3	US-08-474-410-1	Sequence 1, Appli
11	146.6	12.3	1475	3	US-08-486-673B-1	Sequence 1, Appli
12	139.4	11.7	1764	1	US-08-313-553-12	Sequence 12, Appl
13	139.4	11.7	1764	3	US-08-767-993-12	Sequence 12, Appl
14	139.4	11.7	3472	4	US-09-016-434-1328	Sequence 1328, Ap
15	139.4	11.7	3480	1	US-07-657-769B-68	Sequence 68, Appl
16	139.4	11.7	3480	1	US-07-789-184-219	Sequence 219, App

## SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1192	100.0	4206	9	BC043610	BC043610 Homo sapi
c 2	1192	100.0	162377	9	AL683870	AL683870 Human DNA
c 3	1192	100.0	203673	2	BX296528	BX296528 Homo sapi
4	1181	99.1	2137	6	AX147830	AX147830 Sequence
5	1181	99.1	2137	6	AX521879	AX521879 Sequence
6	1181	99.1	2137	6	AX549244	AX549244 Sequence
7	656.2	55.1	1092	9	AB065587	AB065587 Homo sapi
8	656.2	55.1	62466	2	AC083998	AC083998 Homo sapi
c 9	505.4	42.4	507	6	AX147762	AX147762 Sequence
c 10	505.4	42.4	507	6	AX521811	AX521811 Sequence
11	460.2	38.6	856	6	AX646967	AX646967 Sequence
12	458.4	38.5	465	6	AX147804	AX147804 Sequence
13	458.4	38.5	465	6	AX521853	AX521853 Sequence
14	382.2	32.1	599	6	AX378802	AX378802 Sequence
c 15	287.2	24.1	263203	2	BX294188	BX294188 Danio rer
16	196.4	16.5	182064	2	AC130634	AC130634 Rattus no
17	191	16.0	3313	10	BC031516	BC031516 Mus muscu
18	191	16.0	5620	10	MMTHREC02	U36757 Mus musculu

## SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1192	100.0	1192	21	AAA14828	cDNA encoding a hu
2	1192	100.0	1425	25	ABV73368	Human TGR341 polyp
3	1184	99.3	1955	21	AAZ99588	cDNA encoding a hu
4	1181	99.1	2137	22	AAH51006	Human nGPCR5 codin
5	1181	99.1	2137	24	ABS70239	DNA encoding human
6	1180	99.0	2690	25	AAD51227	Human REMAP-8 cDNA
7	1169	98.1	2136	25	ABZ42524	Human LS160435 rec
8	1101.2	92.4	1554	25	ABS57617	Human G protein co
9	1080	90.6	1080	22	AAF57649	Human G-protein co
10	1080	90.6	1080	23	AAI64231	G-protein coupled
11	1078.4	90.5	1080	21	AAD01131	Human orphan G pro
12	1078.4	90.5	1080	21	AAA46032	Human G protein co

c	13	505.4	42.4	507	22	AAH50972	Human nGPCR5 codin
c	14	505.4	42.4	507	24	ABS70205	DNA encoding human
	15	458.4	38.5	465	22	AAH50993	Human nGPCR37 codi
	16	458.4	38.5	465	24	ABS70226	DNA encoding human
	17	382.2	32.1	599	22	AAF57650	Human G-protein co
	18	382.2	32.1	599	23	AAI64232	G-protein coupled
	19	382.2	32.1	599	24	AAS98094	Human DNA for pote
	20	382.2	32.1	599	24	AAS20599	Human P2Y purinoce

# SUMMARIES

Result	No.	Score	% Match	Query Length	DB	ID	Description
	1	451.6	37.9	1201	13	BX365672	BX365672 BX365672
	2	423.2	35.5	836	9	AL582053	AL582053 AL582053
	3	382.2	32.1	599	9	AA804531	AA804531 ns28c04.s
	4	351.4	29.5	769	12	BI262513	BI262513 602953704
	5	335.6	28.2	1071	12	BQ049419	BQ049419 AGENCOURT
	6	248.2	20.8	861	13	BU453416	BU453416 603218165
	7	228	19.1	455	10	BE245598	BE245598 TCBAP1E22
	8	214	18.0	797	14	CA357518	CA357518 629886 NC
	9	209	17.5	766	9	AJ451634	AJ451634 AJ451634
	10	192	16.1	726	13	BU205538	BU205538 604156313
	11	191	16.0	3338	11	AK085990	AK085990 Mus muscu
	12	186.8	15.7	677	29	DR49B19T	AL978032 Danio rer
	13	178.8	15.0	684	14	CA048916	CA048916 ssalsrkc0
	14	173.8	14.6	821	12	BM946931	BM946931 UI-M-EH0p
	15	168.2	14.1	587	14	CB511493	CB511493 ssalrgb53
	16	160.6	13.5	938	29	CNS04SUP	AL305674 Tetraodon
	17	157.6	13.2	769	13	BU702637	BU702637 UI-M-FC0-
	18	155.2	13.0	710	13	BU613761	BU613761 UI-M-EW0-
	19	140.2	11.8	600	14	CA530488	CA530488 9042-47 M
	20	139.6	11.7	739	14	CD493280	CD493280 CDA04-C04
	21	134.6	11.3	556	29	CNS03DLW	AL239261 Tetraodon
c	22	132.8	11.1	817	29	CNS03DLV	AL239260 Tetraodon
	23	129.2	10.8	942	13	BQ896389	BQ896389 AGENCOURT
	24	128.6	10.8	764	14	CB572779	CB572779 AGENCOURT

## RESULT 3

AA804531

LOCUS AA804531 599 bp mRNA linear EST 18-FEB-1998

DEFINITION ns28c04.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1184934 3' similar to TR:P79928 P79928 P2Y8 NUCLEOTIDE RECEPTOR. ;, mRNA sequence.

ACCESSION AA804531

VERSION AA804531.1 GI:2873662

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 599)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Insert Length: 1986 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 420.

FEATURES  
 source Location/Qualifiers  
 1. .599  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1184934"  
 /tissue\_type="germinal center B cell"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI\_CGAP\_GCB1"  
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGCGCCTCATTTTTTTTTTTTTTTT-3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 99 a 195 c 175 g 128 t 2 others  
 ORIGIN

Query Match 32.1%; Score 382.2; DB 9; Length 599;  
 Best Local Similarity 97.5%; Pred. No. 9e-66;  
 Matches 387; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

```

Qy      1 CCCGGGCGAGGACCCCTCCAGGATGCAGGTCCCGAACAGCACCGGCCCGGACAACGCGAC 60
      |||
Db      194 CCCGGGCGAGGACCCCTCCAGGATGCAGGTCCCGAACAGCACCGGCCCGGACAACGCGAC 253

Qy      61 GCTGCAGATGCTGCGGAACCCGGCGATCGCGGTGGCCCTGCCCGTGGTGTACTCGCTGGT 120
      |||
Db      254 GCTGCAGATGCTGCGGAACCCGGCGATCGCGGTGGCCCTGCCCGTGGTGTACTCGCTGGT 313

Qy      121 GGCGGGCGGTGAGCATCCCGGGCAACCTCTTCTCTCTGTGGGTGCTGTGCCGGCGCATGGG 180
      |||
Db      314 GGCGGGCGGTGAGCATCCCGGGCAACCTCTTCTCTCTGTGGGTGCTGTGCCGGCGCATGGG 373

Qy      181 GCCCAGATCCCGTTCGTCATCTTTCATGATCAACCTGAGCGTCACGGACCTGATGCTGGC 240
      |||
Db      374 GCCCAGATCCCGTTCGTCATCTTTCATGATCAACCTGAGCGTCACGGACCTGATGCTGGC 433

Qy      241 CAGCGTGTGGCTTTCCAAATCTACTACCATGCAACCGCCACCACTGGGTATTTCGGGGT 300
      |||
Db      434 CAGCGTGTGGCTTTCCAAATCTACTACCATGCAACCGCCACCACTGGGTATTTCGGGGT 493

Qy      301 GCTGCTTTGCAACGTGGTGACCGTGGCCTTTTACGCAAACATGTATTCCAGCATCCTCAC 360
      |||
Db      494 GCTGCTTTGCAACGTGGTGACCGTGGCCTTTTACGCAAACATGTAGTTTCAGCATNCTCAG 553

Qy      361 CATGACCTGTATCAGCGTGGAGCGCTTCCTGGGGGTC 397
      |||
Db      554 CATGANCTGTATCAGCGTGGAGGCTTCCTTGGGGGTC 590

```

SEQ ID NO: 1 23-1099

SUMMARIES						
Result	% Query					
No.	Score	Match	Length	DB	ID	Description
1	148.2	13.8	2732	1	US-08-476-000-60	Sequence 60, Appl
2	148.2	13.8	2732	1	US-08-472-840-60	Sequence 60, Appl
3	148.2	13.8	2732	2	US-08-476-976-60	Sequence 60, Appl

4	148.2	13.8	2732	3	US-08-474-410-60	Sequence 60, Appl
5	148.2	13.8	2732	3	US-08-486-673B-60	Sequence 60, Appl
6	146.6	13.6	1475	1	US-08-097-938-1	Sequence 1, Appli
7	146.6	13.6	1475	1	US-08-476-000-1	Sequence 1, Appli
8	146.6	13.6	1475	1	US-08-472-840-1	Sequence 1, Appli
9	146.6	13.6	1475	2	US-08-476-976-1	Sequence 1, Appli
10	146.6	13.6	1475	3	US-08-474-410-1	Sequence 1, Appli
11	146.6	13.6	1475	3	US-08-486-673B-1	Sequence 1, Appli
12	139.4	12.9	1764	1	US-08-313-553-12	Sequence 12, Appl
13	139.4	12.9	1764	3	US-08-767-993-12	Sequence 12, Appl
14	139.4	12.9	3472	4	US-09-016-434-1328	Sequence 1328, Ap
15	139.4	12.9	3480	1	US-07-657-769B-68	Sequence 68, Appl
16	139.4	12.9	3480	1	US-07-789-184-219	Sequence 219, App
17	139.4	12.9	3480	1	US-08-475-263-219	Sequence 219, App

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1077	100.0	2137	6	AX147830	AX147830 Sequence
2	1077	100.0	2137	6	AX521879	AX521879 Sequence
3	1077	100.0	2137	6	AX549244	AX549244 Sequence
4	1077	100.0	4206	9	BC043610	BC043610 Homo sapi
c 5	1077	100.0	162377	9	AL683870	AL683870 Human DNA
c 6	1077	100.0	203673	2	BX296528	BX296528 Homo sapi
7	648.4	60.2	1092	9	AB065587	AB065587 Homo sapi
8	648.4	60.2	62466	2	AC083998	AC083998 Homo sapi
c 9	505.4	46.9	507	6	AX147762	AX147762 Sequence
c 10	505.4	46.9	507	6	AX521811	AX521811 Sequence
11	439.4	40.8	465	6	AX147804	AX147804 Sequence
12	439.4	40.8	465	6	AX521853	AX521853 Sequence
13	438.2	40.7	856	6	AX646967	AX646967 Sequence
14	360.2	33.4	599	6	AX378802	AX378802 Sequence
c 15	287	26.6	263203	2	BX294188	BX294188 Danio rer
16	196.4	18.2	182064	2	AC130634	AC130634 Rattus no
17	191	17.7	3313	10	BC031516	BC031516 Mus muscu
18	191	17.7	5620	10	MMTHREC02	U36757 Mus musculu
19	191	17.7	199227	2	AC110876	AC110876 Mus muscu
c 20	191	17.7	235097	2	AC110877	AC110877 Mus muscu
21	190	17.6	3418	10	RATTRGPC	M81642 Rat G-prote
22	181.4	16.8	1312	10	MUSTHRRCT	L03529 Mus musculu
23	178.4	16.6	1164	10	CLU34047	U34047 Cricetulus
24	175.2	16.3	2855	10	CLTHRREC	X61958 C.longicaud

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	429.6	39.9	1201	13	BX365672	BX365672 BX365672
2	405.2	37.6	836	9	AL582053	AL582053 AL582053
3	360.2	33.4	599	9	AA804531	AA804531 ns28c04.s
4	340.4	31.6	769	12	BI262513	BI262513 602953704
5	313.6	29.1	1071	12	BQ049419	BQ049419 AGENCOURT
6	248.2	23.0	861	13	BU453416	BU453416 603218165
7	214	19.9	797	14	CA357518	CA357518 629886 NC
8	209	19.4	766	9	AJ451634	AJ451634 AJ451634
9	206	19.1	455	10	BE245598	BE245598 TCBAPIE22
10	192	17.8	726	13	BU205538	BU205538 604156313
11	191	17.7	3338	11	AK085990	AK085990 Mus muscu
12	186.6	17.3	677	29	DR49B19T	AL978032 Danio rer
13	178.8	16.6	684	14	CA048916	CA048916 ssalsrkc0
14	173.8	16.1	821	12	BM946931	BM946931 UI-M-EH0p
15	168.2	15.6	587	14	CB511493	CB511493 ssalrgb53
16	160.6	14.9	938	29	CNS04SUP	AL305674 Tetraodon
17	157.6	14.6	769	13	BU702637	BU702637 UI-M-FC0-

RESULT 3

AA804531

LOCUS AA804531 599 bp mRNA linear EST 18-FEB-1998  
 DEFINITION ns28c04.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1184934 3' similar to TR:P79928 P79928 P2Y8 NUCLEOTIDE RECEPTOR. ;, mRNA sequence.

ACCESSION AA804531

VERSION AA804531.1 GI:2873662

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 599)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)

Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Insert Length: 1986 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 420.

FEATURES

source

Location/Qualifiers

1..599

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1184934"

/tissue\_type="germinal center B cell"

/lab\_host="DH10B"

/clone\_lib="NCI\_CGAP\_GCB1"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGCGCCTCATTTTTTTTTTTTTTTTT-3']

. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 99 a 195 c 175 g 128 t 2 others

ORIGIN

Query Match 33.4%; Score 360.2; DB 9; Length 599;

Best Local Similarity 97.3%; Pred. No. 1.7e-62;

Matches 365; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 ATGCAGGTCCCGAACAGCACCAGCGCCCGGACAACGCGACGCTGCAGATGCTGCGGAACCCG 60  
 |||  
 Db 216 ATGCAGGTCCCGAACAGCACCAGCGCCCGGACAACGCGACGCTGCAGATGCTGCGGAACCCG 275  
 Qy 61 GCGATCGCGGTGGCCCTGCCCGTGGTGTACTCGCTGGTGGCGGCGGTCAGCATCCCGGGC 120  
 |||  
 Db 276 GCGATCGCGGTGGCCCTGCCCGTGGTGTACTCGCTGGTGGCGGCGGTCAGCATCCCGGGC 335  
 Qy 121 AACCTCTTCTCTCTGTGGGTGCTGTGCCGGCGCATGGGGCCAGATCCCCGTCGGTCATC 180  
 |||

Db 336 AACCTCTTCTCTGTGGGTGCTGTGCCGGCGCATGGGGCCCAGATCCCCGTCGGTCATC 395  
 Qy 181 TTCATGATCAACCTGAGCGTCACGGACCTGATGCTGGCCAGCGTGTGCCTTTCCAAATC 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 396 TTCATGATCAACCTGAGCGTCACGGACCTGATGCTGGCCAGCGTGTGCCTTTCCAAATC 455  
 Qy 241 TACTACCATTGCAACCGCCACCACTGGGTATTTCGGGGTGCTGCTTTGCAACGTGGTGACC 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 456 TACTACCATTGCAACCGCCACCACTGGGTATTTCGGGGTGCTGCTTTGCAACGTGGTGACC 515  
 Qy 301 GTGGCCTTTTACGCAAACATGTATTCCAGCATCCTCACCATGACCTGTATCAGCGTGGAG 360  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 516 GTGGCCTTTTACGCAAACATGTAGTTCAGCATNCTCAGCATGANCTGTATCAGCGTGGAG 575  
 Qy 361 CGCTTCCTGGGGGTC 375  
 |||||||||  
 Db 576 GCTTCCTTGGGGGTC 590